

## WEST Search History

DATE: Wednesday, May 17, 2006

Hide?	Set Name	Query	Hit Count
		<i>DB=USPT; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L1	pro211	47

END OF SEARCH HISTORY

# SCORE Search Results Details for Application 09903749 and Search Result us-09-903-749a- 2.rapbn.

[Score Home](#)    [Retrieve Application](#)    [SCORE System](#)    [SCORE](#)    [Comments /](#)  
[Page](#)    [List](#)    [Overview](#)    [FAQ](#)    [Suggestions](#)

This page gives you Search Results detail for the Application 09903749 and Search Result us-09-903-749a-2.rapbn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 21:19:57 ; Search time 28 Seconds  
(without alignments)  
591.891 Million cell updates/sec

Title: US-09-903-749A-2  
Perfect score: 2005  
Sequence: 1 MRLPRRAALGLLPLLLLLPP.....AEAEATEGESPTQLPSREDL 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications AA\_New:\*  
1: /SIDS5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep1:\*  
2: /SIDS5/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /SIDS5/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /SIDS5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /SIDS5/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /SIDS5/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
7: /SIDS5/ptodata/1/pubpaa/US09\_NEW\_PUB.pep1:\*  
8: /SIDS5/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
9: /SIDS5/ptodata/1/pubpaa/US10\_NEW\_PUB.pep1:\*  
10: /SIDS5/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
11: /SIDS5/ptodata/1/pubpaa/US11\_NEW\_PUB.pep1:\*  
12: /SIDS5/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	2005	100.0	353	9 US-10-131-826A-296	Sequence 296, App
2	2005	100.0	353	9 US-10-973-115B-296	Sequence 296, App
3	2005	100.0	353	9 US-10-137-873A-296	Sequence 296, App
4	2005	100.0	353	9 US-10-152-370-296	Sequence 296, App
5	2005	100.0	353	11 US-11-290-153-296	Sequence 296, App

6	1787	89.1	391	9	US-10-784-004-1228	Sequence 1228, Ap
7	971.5	48.5	420	9	US-10-131-826A-290	Sequence 290, App
8	971.5	48.5	420	9	US-10-973-115B-290	Sequence 290, App
9	971.5	48.5	420	9	US-10-218-784-122	Sequence 122, App
10	971.5	48.5	420	9	US-10-219-061-122	Sequence 122, App
11	971.5	48.5	420	9	US-10-219-062-122	Sequence 122, App
12	971.5	48.5	420	9	US-10-219-064-122	Sequence 122, App
13	971.5	48.5	420	9	US-10-233-134-122	Sequence 122, App
14	971.5	48.5	420	9	US-10-137-873A-290	Sequence 290, App
15	971.5	48.5	420	9	US-10-152-370-290	Sequence 290, App
16	971.5	48.5	420	11	US-11-290-153-290	Sequence 290, App
17	277.5	13.8	1416	11	US-11-128-059-60	Sequence 60, Appl
18	277.5	13.8	1494	11	US-11-128-059-78	Sequence 78, Appl
19	277.5	13.8	2086	11	US-11-128-059-82	Sequence 82, Appl
20	277.5	13.8	2313	11	US-11-128-059-80	Sequence 80, Appl
21	277.5	13.8	2358	11	US-11-128-059-74	Sequence 74, Appl
22	277.5	13.8	2439	11	US-11-128-059-76	Sequence 76, Appl
23	277.5	13.8	2458	11	US-11-128-059-94	Sequence 94, Appl
24	277.5	13.8	2551	9	US-10-453-372-256	Sequence 256, App
25	277.5	13.8	2551	11	US-11-128-059-96	Sequence 96, Appl
26	268.5	13.4	2871	11	US-11-169-041-131	Sequence 131, App
27	268.5	13.4	3002	9	US-10-821-234-916	Sequence 916, App
28	268	13.4	1821	8	US-10-505-928-451	Sequence 451, App
29	254.5	12.7	566	11	US-11-065-695-2	Sequence 2, Appli
30	254.5	12.7	601	11	US-11-065-695-8	Sequence 8, Appli
31	254.5	12.7	652	9	US-10-821-234-1016	Sequence 1016, Ap
32	254.5	12.7	683	11	US-11-065-695-6	Sequence 6, Appli
33	254.5	12.7	703	9	US-10-821-234-1412	Sequence 1412, Ap
34	254.5	12.7	703	11	US-11-065-695-4	Sequence 4, Appli
35	254	12.7	533	11	US-11-128-059-58	Sequence 58, Appl
36	253	12.6	1323	11	US-11-128-059-92	Sequence 92, Appl
37	253	12.6	1327	11	US-11-128-059-84	Sequence 84, Appl
38	253	12.6	1416	11	US-11-128-059-4	Sequence 4, Appli
39	253	12.6	1502	9	US-10-453-372-252	Sequence 252, App
40	253	12.6	1510	9	US-10-453-372-254	Sequence 254, App
41	253	12.6	2417	9	US-10-453-372-228	Sequence 228, App
42	250	12.5	3623	9	US-10-995-561-593	Sequence 593, App
43	249.5	12.4	2911	11	US-11-090-617-706	Sequence 706, App
44	247	12.3	997	11	US-11-113-424-37	Sequence 37, Appl
45	244	12.2	999	11	US-11-113-424-36	Sequence 36, Appl
46	242.5	12.1	1184	11	US-11-065-695-10	Sequence 10, Appl
47	240.5	12.0	1400	9	US-10-821-234-1045	Sequence 1045, Ap
48	238	11.9	509	8	US-10-196-749-52	Sequence 52, Appl
49	238	11.9	509	9	US-10-194-487-52	Sequence 52, Appl
50	238	11.9	509	9	US-10-195-883-52	Sequence 52, Appl
51	238	11.9	509	9	US-10-195-888-52	Sequence 52, Appl
52	238	11.9	509	9	US-10-195-889-52	Sequence 52, Appl
53	238	11.9	509	11	US-11-124-327-2	Sequence 2, Appli
54	238	11.9	536	9	US-10-453-372-30	Sequence 30, Appl
55	238	11.9	542	9	US-10-453-372-10	Sequence 10, Appl
56	238	11.9	964	11	US-11-137-465-58	Sequence 58, Appl
57	238	11.9	965	11	US-11-113-424-2	Sequence 2, Appli
58	238	11.9	965	11	US-11-147-047-51	Sequence 51, Appl
59	238	11.9	997	11	US-11-080-991-50	Sequence 50, Appl
60	237	11.8	536	9	US-10-453-372-6	Sequence 6, Appli
61	237	11.8	536	9	US-10-453-372-22	Sequence 22, Appl
62	237	11.8	536	9	US-10-453-372-24	Sequence 24, Appl
63	237	11.8	536	9	US-10-453-372-26	Sequence 26, Appl
64	236	11.8	536	9	US-10-453-372-28	Sequence 28, Appl
65	236	11.8	961	11	US-11-113-424-35	Sequence 35, Appl
66	234.5	11.7	572	9	US-10-453-372-16	Sequence 16, Appl
67	232	11.6	552	9	US-10-453-372-14	Sequence 14, Appl
68	232	11.6	1375	9	US-10-995-561-809	Sequence 809, App
69	232	11.6	1376	11	US-11-100-640-32	Sequence 32, Appl
70	231.5	11.5	204	9	US-10-453-372-18	Sequence 18, Appl
71	231.5	11.5	204	9	US-10-453-372-20	Sequence 20, Appl
72	231.5	11.5	421	9	US-10-453-372-220	Sequence 220, App
73	231.5	11.5	533	9	US-10-453-372-230	Sequence 230, App
74	231.5	11.5	533	9	US-10-453-372-232	Sequence 232, App
75	231.5	11.5	552	9	US-10-453-372-234	Sequence 234, App
76	231.5	11.5	552	9	US-10-453-372-238	Sequence 238, App
77	231.5	11.5	552	9	US-10-453-372-242	Sequence 242, App
78	231.5	11.5	552	9	US-10-453-372-244	Sequence 244, App
79	231.5	11.5	552	9	US-10-453-372-246	Sequence 246, App
80	231.5	11.5	552	9	US-10-453-372-248	Sequence 248, App
81	231.5	11.5	552	9	US-10-453-372-250	Sequence 250, App

# SCORE Search Results Details for Application 09903749 and Search Result us-09-903-749a- 2.ra1.

[Score Home](#)    [Retrieve Application](#)    [SCORE System](#)    [SCORE](#)    [Comments /](#)  
[Page](#)    [List](#)    [Overview](#)    [FAQ](#)    [Suggestions](#)

This page gives you Search Results detail for the Application 09903749 and Search Result us-09-903-749a-2.ra1.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 21:00:31 ; Search time 25 Seconds  
(without alignments)  
1167.381 Million cell updates/sec

Title: US-09-903-749A-2  
Perfect score: 2005  
Sequence: 1 MRLPRRAALGLLPLLLLPP.....AEAEATEGESPTQLPSREDL 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	2005	100.0		353	2	US-09-907-794A-2	Sequence 2, Appli
2	2005	100.0		353	2	US-09-905-125A-2	Sequence 2, Appli
3	2005	100.0		353	2	US-09-902-775A-2	Sequence 2, Appli
4	2005	100.0		353	2	US-09-906-700-2	Sequence 2, Appli
5	2005	100.0		353	2	US-09-903-603A-2	Sequence 2, Appli
6	2005	100.0		353	2	US-09-904-920A-2	Sequence 2, Appli
7	2005	100.0		353	2	US-09-909-064-2	Sequence 2, Appli
8	2005	100.0		353	2	US-09-905-381A-2	Sequence 2, Appli
9	2005	100.0		353	2	US-09-906-618-2	Sequence 2, Appli
10	2005	100.0		353	2	US-09-906-646-2	Sequence 2, Appli
11	2005	100.0		353	2	US-09-904-462-2	Sequence 2, Appli

12	2005	100.0	353	2	US-09-902-736A-2	Sequence 2, Appli
13	2005	100.0	353	2	US-09-906-722A-2	Sequence 2, Appli
14	2005	100.0	353	2	US-10-188-495-56	Sequence 56, Appl
15	1887	94.1	329	2	US-10-188-495-58	Sequence 58, Appl
16	1481.5	73.9	348	2	US-10-188-495-69	Sequence 69, Appl
17	971.5	48.5	420	2	US-09-907-794A-109	Sequence 109, App
18	971.5	48.5	420	2	US-09-905-125A-109	Sequence 109, App
19	971.5	48.5	420	2	US-09-902-775A-109	Sequence 109, App
20	971.5	48.5	420	2	US-09-906-700-109	Sequence 109, App
21	971.5	48.5	420	2	US-09-903-603A-109	Sequence 109, App
22	971.5	48.5	420	2	US-09-904-920A-109	Sequence 109, App
23	971.5	48.5	420	2	US-09-909-064-109	Sequence 109, App
24	971.5	48.5	420	2	US-09-905-381A-109	Sequence 109, App
25	971.5	48.5	420	2	US-09-906-618-109	Sequence 109, App
26	971.5	48.5	420	2	US-09-906-646-109	Sequence 109, App
27	971.5	48.5	420	2	US-09-904-462-109	Sequence 109, App
28	971.5	48.5	420	2	US-09-902-736A-109	Sequence 109, App
29	971.5	48.5	420	2	US-09-906-722A-109	Sequence 109, App
30	860.5	42.9	392	2	US-10-144-929-156	Sequence 156, App
31	670	33.4	777	2	US-09-270-767-44409	Sequence 44409, A
32	463.5	23.1	242	2	US-09-312-283C-393	Sequence 393, App
33	277.5	13.8	1581	2	US-09-949-002-414	Sequence 414, App
34	272	13.6	1587	2	US-09-949-002-354	Sequence 354, App
35	268.5	13.4	1935	2	US-09-949-016-10403	Sequence 10403, A
36	268.5	13.4	2871	2	US-09-538-092-1076	Sequence 1076, Ap
37	268	13.4	1656	2	US-09-949-016-7247	Sequence 7247, Ap
38	268	13.4	1821	2	US-09-949-016-5938	Sequence 5938, Ap
39	256	12.8	77	2	US-09-621-976-4010	Sequence 4010, Ap
40	255.5	12.7	1253	2	US-08-479-722B-4	Sequence 4, Appli
41	255.5	12.7	1253	2	US-09-592-685-4	Sequence 4, Appli
42	254.5	12.7	575	2	US-09-949-016-11264	Sequence 11264, A
43	254.5	12.7	575	2	US-09-949-016-11265	Sequence 11265, A
44	254.5	12.7	575	2	US-09-949-016-11266	Sequence 11266, A
45	254.5	12.7	575	2	US-09-949-016-11267	Sequence 11267, A
46	254.5	12.7	652	1	US-08-751-305-2	Sequence 2, Appli
47	254.5	12.7	657	2	US-09-949-016-11365	Sequence 11365, A
48	254.5	12.7	657	2	US-09-949-016-11366	Sequence 11366, A
49	254.5	12.7	657	2	US-09-949-016-11367	Sequence 11367, A
50	254.5	12.7	657	2	US-09-949-016-11368	Sequence 11368, A
51	254.5	12.7	677	2	US-09-949-016-11369	Sequence 11369, A
52	254.5	12.7	677	2	US-09-949-016-11370	Sequence 11370, A
53	254.5	12.7	677	2	US-09-949-016-11371	Sequence 11371, A
54	254.5	12.7	677	2	US-09-949-016-11372	Sequence 11372, A
55	250	12.5	1833	2	US-08-479-722B-2	Sequence 2, Appli
56	250	12.5	1833	2	US-09-592-685-2	Sequence 2, Appli
57	250	12.5	1833	4	PCT-US95-02251-18	Sequence 18, Appl
58	248	12.4	1106	2	US-09-949-016-9626	Sequence 9626, Ap
59	247	12.3	997	2	US-09-747-371-3	Sequence 3, Appli
60	246.5	12.3	1251	4	PCT-US95-02251-3	Sequence 3, Appli
61	246.5	12.3	1252	1	US-08-199-780-3	Sequence 3, Appli
62	246.5	12.3	1252	1	US-08-316-650-3	Sequence 3, Appli
63	246	12.3	140	2	US-09-270-767-59840	Sequence 59840, A
64	244	12.2	999	2	US-09-747-371-2	Sequence 2, Appli
65	240.5	12.0	996	2	US-09-949-016-8254	Sequence 8254, Ap
66	240.5	12.0	1394	2	US-09-949-016-5971	Sequence 5971, Ap
67	240.5	12.0	1394	6	5177197-30	Patent No. 5177197
68	239	11.9	676	1	US-08-282-141-4	Sequence 4, Appli
69	239	11.9	676	1	US-08-435-434-3	Sequence 3, Appli
70	239	11.9	676	1	US-08-435-436-3	Sequence 3, Appli
71	239	11.9	676	1	US-08-438-863-3	Sequence 3, Appli
72	239	11.9	676	1	US-08-438-864-3	Sequence 3, Appli
73	239	11.9	676	2	US-08-438-862-3	Sequence 3, Appli
74	239	11.9	676	2	US-08-628-747-3	Sequence 3, Appli
75	239	11.9	676	2	US-08-402-253-3	Sequence 3, Appli
76	239	11.9	676	2	US-08-443-866B-3	Sequence 3, Appli
77	238	11.9	509	2	US-09-907-794A-315	Sequence 315, App
78	238	11.9	509	2	US-09-905-125A-315	Sequence 315, App
79	238	11.9	509	2	US-09-902-775A-315	Sequence 315, App
80	238	11.9	509	2	US-09-906-700-315	Sequence 315, App
81	238	11.9	509	2	US-09-903-603A-315	Sequence 315, App
82	238	11.9	509	2	US-09-904-920A-315	Sequence 315, App
83	238	11.9	509	2	US-09-909-064-315	Sequence 315, App
84	238	11.9	509	2	US-09-905-381A-315	Sequence 315, App
85	238	11.9	509	2	US-09-906-618-315	Sequence 315, App
86	238	11.9	509	2	US-09-906-646-315	Sequence 315, App
87	238	11.9	509	2	US-09-904-462-315	Sequence 315, App

# SCORE Search Results Details for Application 09903749 and Search Result us-09-903-749a-2.rup.

[Score Home](#)    [Retrieve Application](#)    [SCORE System](#)    [SCORE](#)    [Comments /](#)  
[Page](#)    [List](#)    [Overview](#)    [FAQ](#)    [Suggestions](#)

This page gives you Search Results detail for the Application 09903749 and Search Result us-09-903-749a-2.rup.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 21:01:41 ; Search time 231 Seconds  
(without alignments)  
1078.145 Million cell updates/sec

Title: US-09-903-749A-2  
Perfect score: 2005  
Sequence: 1 MRLPRRAALGLLPLLLLPP.....AEAEATEGESPTQLPSREDL 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2005	100.0	353	2	Q6UXH1_HUMAN	Q6uxh1 homo sapien
2	1995	99.5	353	2	Q86UC0_HUMAN	Q86uc0 homo sapien
3	1787	89.1	321	2	Q9BU47_HUMAN	Q9bu47 homo sapien
4	1553	77.5	349	2	Q4G063_RAT	Q4g063 rattus norv
5	1533.5	76.5	350	2	Q9CYA0_MOUSE	Q9cya0 mus musculus
6	1481.5	73.9	348	2	Q60438_CRIGR	Q60438 cricetus
7	1465	73.1	284	2	Q4W0V0_HUMAN	Q4w0v0 homo sapien
8	1209	60.3	361	2	Q5XH36_XENLA	Q5xh36 xenopus lae
9	1184	59.1	361	2	Q4V7M2_XENLA	Q4v7m2 xenopus lae
10	1058	52.8	296	2	Q4STE9_TETNG	Q4ste9 tetraodon n
11	1020.5	50.9	341	2	Q7SXF6_BRARE	Q7sxf6 brachydanio
12	1019.5	50.8	341	2	Q5RFU8_BRARE	Q5rfu8 brachydanio
13	992.5	49.5	408	2	Q58CS1_BOVIN	Q58cs1 bos taurus
14	992.5	49.5	420	2	Q5EA46_BOVIN	Q5ea46 bos taurus
15	981	48.9	420	2	Q4V7F2_RAT	Q4v7f2 rattus norv

16	971.5	48.5	420	2	Q8NFT4_HUMAN	Q8nft4	homo sapien
17	969	48.3	422	2	Q96HD1_HUMAN	Q96hd1	homo sapien
18	968.5	48.3	420	2	Q91XD7_MOUSE	Q91xd7	mus musculus
19	959.5	47.9	417	2	Q9Y409_HUMAN	Q9y409	homo sapien
20	950	47.4	422	2	Q6I9X5_HUMAN	Q6i9x5	homo sapien
21	844	42.1	367	2	Q4RJU5_TETNG	Q4rju5	tetraodon n
22	699	34.9	124	2	Q659B4_HUMAN	Q659b4	homo sapien
23	670	33.4	374	2	Q9VPJ0_DROME	Q9vpj0	drosophila
24	661	33.0	391	2	Q5TQL0_ANOGA	Q5tql0	anopheles g
25	643.5	32.1	319	2	Q7Q3P0_ANOGA	Q7q3p0	anopheles g
26	599.5	29.9	165	2	Q9DFE9_ONCMY	Q9dfe9	oncorhynch
27	540	26.9	356	2	Q19267_CAEEL	Q19267	caenorhabdi
28	519	25.9	358	2	Q623K4_CAEBR	Q623k4	caenorhabdi
29	423	21.1	172	2	Q8BY28_MOUSE	Q8by28	m mus muscu
30	296.5	14.8	536	2	Q5RG03_BRARE	Q5rg03	brachydanio
31	286.5	14.3	704	1	FBLN1_CHICK	Q73775	gallus gall
32	279.5	13.9	937	2	Q9BLJ1_CIOIN	Q9blj1	ciona intes
33	279	13.9	2360	2	Q7YZP0_EIMMA	Q7yzp0	eimeria max
34	277.5	13.8	2551	1	STAB2_HUMAN	Q8wwq8	h stabilin-
35	276.5	13.8	1431	1	STAB2_RAT	Q8cfm6	rattus norv
36	274.5	13.7	2559	1	STAB2_MOUSE	Q8r4u0	mus musculus
37	274.5	13.7	2871	1	FBN1_PIG	Q9tv36	sus scrofa
38	272	13.6	1587	2	O00508_HUMAN	O00508	homo sapien
39	271.5	13.5	1511	2	O75412_HUMAN	O75412	homo sapien
40	271	13.5	2189	2	Q9BI05_EIMTE	Q9bi05	eimeria ten
41	270.5	13.5	3857	2	O88840_MOUSE	O88840	mus musculus
42	270	13.5	2871	1	FBN1_BOVIN	P98133	bos taurus
43	269.5	13.4	3864	2	Q61MD6_CAEBR	Q61md6	caenorhabdi
44	268.5	13.4	2871	1	FBN1_HUMAN	P35555	homo sapien
45	268.5	13.4	2871	2	Q75N87_HUMAN	Q75n87	homo sapien
46	268	13.4	1700	2	Q59EE6_HUMAN	Q59ee6	homo sapien
47	268	13.4	1821	1	LTBP2_HUMAN	Q14767	homo sapien
48	268	13.4	1821	2	Q6AZ94_HUMAN	Q6az94	homo sapien
49	266.5	13.3	644	1	C1QR1_MOUSE	O89103	mus musculus
50	266.5	13.3	1666	1	LTBP4_MOUSE	Q8k4g1	mus musculus
51	264.5	13.2	1560	2	Q5JSG7_HUMAN	Q5jsg7	homo sapien
52	264.5	13.2	2809	1	FBN3_HUMAN	Q75n90	homo sapien
53	264	13.2	1842	1	LTBP2_BOVIN	Q28019	bos taurus
54	263	13.1	567	2	Q4RZ38_TETNG	Q4rz38	tetraodon n
55	263	13.1	708	2	P87363_CHICK	P87363	gallus gall
56	263	13.1	1877	1	PCSK5_MOUSE	Q04592	mus musculus
57	262.5	13.1	1167	2	Q6KAT1_MOUSE	Q6kat1	mus musculus
58	262.5	13.1	1764	1	LTBP2_RAT	O35806	rattus norv
59	262.5	13.1	2872	2	Q9WUH8_RAT	Q9wuh8	rattus norv
60	260.5	13.0	669	2	O75441_HUMAN	O75441	homo sapien
61	260.5	13.0	2884	2	Q4SHN1_TETNG	Q4shn1	tetraodon n
62	260.5	13.0	23015	2	Q8IQ18_DROME	Q8iq18	drosophila
63	260	13.0	754	2	Q5TNY8_ANOGA	Q5tny8	anopheles g
64	259.5	12.9	893	2	Q8MJK0_CERAE	Q8mjk0	cercopithec
65	257.5	12.8	652	2	Q8IXK1_HUMAN	Q8ixk1	homo sapien
66	256.5	12.8	652	1	C1QR1_HUMAN	Q9npy3	homo sapien
67	256.5	12.8	671	2	Q59EB6_HUMAN	Q59eb6	homo sapien
68	256.5	12.8	705	1	FBLN1_MOUSE	Q08879	mus musculus
69	256.5	12.8	1302	1	LTBP3_HUMAN	Q9ns15	homo sapien
70	256	12.8	1268	1	LTBP3_MOUSE	Q61810	mus musculus
71	255	12.7	2532	2	Q629H6_CAEBR	Q629h6	caenorhabdi
72	254.5	12.7	703	1	FBLN1_HUMAN	P23142	homo sapien
73	254	12.7	643	1	C1QR1_RAT	Q9et61	rattus norv
74	253.5	12.6	917	2	Q9V4B8_DROME	Q9v4b8	drosophila
75	253	12.6	2585	2	Q23587_CAEEL	Q23587	caenorhabdi
76	252.5	12.6	2871	1	FBN1_MOUSE	Q61554	mus musculus
77	252.5	12.6	2907	1	FBN2_MOUSE	Q61555	mus musculus
78	252	12.6	1976	2	Q4RT51_TETNG	Q4rt51	tetraodon n
79	252	12.6	3623	2	Q5VTA6_HUMAN	Q5vta6	homo sapien
80	251.5	12.5	941	2	Q54YP0_DICDI	Q54yp0	dictyosteli
81	251.5	12.5	1174	2	Q99K58_MOUSE	Q99k58	mus musculus
82	250.5	12.5	403	2	Q4R3X4_MACFA	Q4r3x4	macaca fasc
83	250.5	12.5	2225	2	Q571J3_MOUSE	Q571j3	mus musculus
84	250	12.5	569	2	Q7PMF9_ANOGA	Q7pmf9	anopheles g
85	250	12.5	1813	1	LTBP2_MOUSE	O08999	mus musculus
86	250	12.5	2571	1	STAB1_MOUSE	Q8r4y4	mus musculus
87	250	12.5	3494	2	Q7LC53_HUMAN	Q7lc53	homo sapien
88	250	12.5	3623	2	O60494_HUMAN	O60494	homo sapien
89	249.5	12.4	2911	1	FBN2_HUMAN	P35556	homo sapien
90	249	12.4	2906	2	Q9WUH9_RAT	Q9wuh9	rattus norv
91	248.5	12.4	1696	1	PCSK5_BRACL	Q9nj15	branchiosto

# SCORE Search Results Details for Application 09903749 and Search Result us-09-903-749a-2.rup.

[Score Home Page](#)
[Retrieve Application List](#)
[SCORE System Overview](#)
[SCORE FAQ](#)
[Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09903749 and Search Result us-09-903-749a-2.rup.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 15, 2006, 21:01:41 ; Search time 231 Seconds  
(without alignments)  
1078.145 Million cell updates/sec

Title: US-09-903-749A-2  
Perfect score: 2005  
Sequence: 1 MRLPRRAALGLLPLLLLLPP.....AEAEATEGESPTQLPSREDL 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2005	100.0	353	2	Q6UXH1_HUMAN	Q6uxh1 homo sapien
2	1995	99.5	353	2	Q86UC0_HUMAN	Q86uc0 homo sapien
3	1787	89.1	321	2	Q9BU47_HUMAN	Q9bu47 homo sapien
4	1553	77.5	349	2	Q4G063_RAT	Q4g063 rattus norv
5	1533.5	76.5	350	2	Q9CYA0_MOUSE	Q9cya0 mus musculu
6	1481.5	73.9	348	2	Q60438_CRIGR	Q60438 cricetulus
7	1465	73.1	284	2	Q4W0V0_HUMAN	Q4w0v0 homo sapien
8	1209	60.3	361	2	Q5XH36_XENLA	Q5xh36 xenopus lae
9	1184	59.1	361	2	Q4V7M2_XENLA	Q4v7m2 xenopus lae
10	1058	52.8	296	2	Q4STE9_TETNG	Q4ste9 tetraodon n
11	1020.5	50.9	341	2	Q7SXF6_BRARE	Q7sxf6 brachydanio
12	1019.5	50.8	341	2	Q5RFU8_BRARE	Q5rfu8 brachydanio
13	992.5	49.5	408	2	Q58CS1_BOVIN	Q58cs1 bos taurus
14	992.5	49.5	420	2	Q5EA46_BOVIN	Q5ea46 bos taurus
15	981	48.9	420	2	Q4V7F2_RAT	Q4v7f2 rattus norv

16	971.5	48.5	420	2	Q8NFT4_HUMAN	Q8nft4	homo sapien
17	969	48.3	422	2	Q96HD1_HUMAN	Q96hd1	homo sapien
18	968.5	48.3	420	2	Q91XD7_MOUSE	Q91xd7	mus musculus
19	959.5	47.9	417	2	Q9Y409_HUMAN	Q9y409	homo sapien
20	950	47.4	422	2	Q619X5_HUMAN	Q619x5	homo sapien
21	844	42.1	367	2	Q4RJU5_TETNG	Q4rju5	tetraodon n
22	699	34.9	124	2	Q659B4_HUMAN	Q659b4	homo sapien
23	670	33.4	374	2	Q9VPJ0_DROME	Q9vpj0	drosophila
24	661	33.0	391	2	Q5TQL0_ANOGA	Q5tql0	anopheles g
25	643.5	32.1	319	2	Q7Q3P0_ANOGA	Q7q3p0	anopheles g
26	599.5	29.9	165	2	Q9DFE9_ONCMY	Q9dfe9	oncorhynchus
27	540	26.9	356	2	Q19267_CAEEL	Q19267	caenorhabditis
28	519	25.9	358	2	Q623K4_CAEEL	Q623k4	caenorhabditis
29	423	21.1	172	2	Q8BY28_MOUSE	Q8by28	mus musculus
30	296.5	14.8	536	2	Q5RG03_BRARE	Q5rg03	brachydanio
31	286.5	14.3	704	1	FBLN1_CHICK	O73775	gallus gall
32	279.5	13.9	937	2	Q9BLJ1_CIOIN	Q9blj1	ciona intes
33	279	13.9	2360	2	Q7YZP0_EIMMA	Q7yzp0	eimeria max
34	277.5	13.8	2551	1	STAB2_HUMAN	Q8wwq8	homo sapien
35	276.5	13.8	1431	1	STAB2_RAT	Q8cfm6	rattus norv
36	274.5	13.7	2559	1	STAB2_MOUSE	Q8r4u0	mus musculus
37	274.5	13.7	2871	1	FBN1_PIG	Q9tv36	sus scrofa
38	272	13.6	1587	2	O00508_HUMAN	O00508	homo sapien
39	271.5	13.5	1511	2	O75412_HUMAN	O75412	homo sapien
40	271	13.5	2189	2	Q9BI05_EIMTE	Q9bi05	eimeria ten
41	270.5	13.5	3857	2	O88840_MOUSE	O88840	mus musculus
42	270	13.5	2871	1	FBN1_BOVIN	P98133	bos taurus
43	269.5	13.4	3864	2	Q61MD6_CAEEL	Q61md6	caenorhabditis
44	268.5	13.4	2871	1	FBN1_HUMAN	P35555	homo sapien
45	268.5	13.4	2871	2	Q75N87_HUMAN	Q75n87	homo sapien
46	268	13.4	1700	2	Q59EE6_HUMAN	Q59ee6	homo sapien
47	268	13.4	1821	1	LTBP2_HUMAN	Q14767	homo sapien
48	268	13.4	1821	2	Q6AZ94_HUMAN	Q6az94	homo sapien
49	266.5	13.3	644	1	C1QR1_MOUSE	O89103	mus musculus
50	266.5	13.3	1666	1	LTBP4_MOUSE	Q8k4g1	mus musculus
51	264.5	13.2	1560	2	Q5JSG7_HUMAN	Q5jsg7	homo sapien
52	264.5	13.2	2809	1	FBN3_HUMAN	Q75n90	homo sapien
53	264	13.2	1842	1	LTBP2_BOVIN	Q28019	bos taurus
54	263	13.1	567	2	Q4RZ38_TETNG	Q4rz38	tetraodon n
55	263	13.1	708	2	P87363_CHICK	P87363	gallus gall
56	263	13.1	1877	1	PCSK5_MOUSE	Q04592	mus musculus
57	262.5	13.1	1167	2	Q6KAT1_MOUSE	Q6kat1	mus musculus
58	262.5	13.1	1764	1	LTBP2_RAT	O35806	rattus norv
59	262.5	13.1	2872	2	Q9WUH8_RAT	Q9wuh8	rattus norv
60	260.5	13.0	669	2	O75441_HUMAN	O75441	homo sapien
61	260.5	13.0	2884	2	Q4SHN1_TETNG	Q4shn1	tetraodon n
62	260.5	13.0	23015	2	Q8IQ18_DROME	Q8iq18	drosophila
63	260	13.0	754	2	Q5TNY8_ANOGA	Q5tny8	anopheles g
64	259.5	12.9	893	2	Q8MJK0_CERAE	Q8mjk0	cercopithec
65	257.5	12.8	652	2	Q8IXK1_HUMAN	Q8ixk1	homo sapien
66	256.5	12.8	652	1	C1QR1_HUMAN	Q9npy3	homo sapien
67	256.5	12.8	671	2	Q59EB6_HUMAN	Q59eb6	homo sapien
68	256.5	12.8	705	1	FBLN1_MOUSE	Q08879	mus musculus
69	256.5	12.8	1302	1	LTBP3_HUMAN	Q9ns15	homo sapien
70	256	12.8	1268	1	LTBP3_MOUSE	Q61810	mus musculus
71	255	12.7	2532	2	Q629H6_CAEEL	Q629h6	caenorhabditis
72	254.5	12.7	703	1	FBLN1_HUMAN	P23142	homo sapien
73	254	12.7	643	1	C1QR1_RAT	Q9et61	rattus norv
74	253.5	12.6	917	2	Q9V4B8_DROME	Q9v4b8	drosophila
75	253	12.6	2585	2	Q23587_CAEEL	Q23587	caenorhabditis
76	252.5	12.6	2871	1	FBN1_MOUSE	Q61554	mus musculus
77	252.5	12.6	2907	1	FBN2_MOUSE	Q61555	mus musculus
78	252	12.6	1976	2	Q4RT51_TETNG	Q4rt51	tetraodon n
79	252	12.6	3623	2	Q5VTA6_HUMAN	Q5vta6	homo sapien
80	251.5	12.5	941	2	Q54YP0_DICTDI	Q54yp0	dictyosteli
81	251.5	12.5	1174	2	Q99K58_MOUSE	Q99k58	mus musculus
82	250.5	12.5	403	2	Q4R3X4_MACFA	Q4r3x4	macaca fasc
83	250.5	12.5	2225	2	Q571J3_MOUSE	Q571j3	mus musculus
84	250	12.5	569	2	Q7PMF9_ANOGA	Q7pmf9	anopheles g
85	250	12.5	1813	1	LTBP2_MOUSE	O08999	mus musculus
86	250	12.5	2571	1	STAB1_MOUSE	Q8r4y4	mus musculus
87	250	12.5	3494	2	Q7LC53_HUMAN	Q7lc53	homo sapien
88	250	12.5	3623	2	O60494_HUMAN	O60494	homo sapien
89	249.5	12.4	2911	1	FBN2_HUMAN	P35556	homo sapien
90	249	12.4	2906	2	Q9WUH9_RAT	Q9wuh9	rattus norv
91	248.5	12.4	1696	1	PCSK5_BRACL	Q9nj15	branchiosto

=> s pro211

L1 21 PRO211

=> s l1 and py=<1997

1 FILES SEARCHED...

L2 8 L1 AND PY=<1997

=> d his

(FILE 'HOME' ENTERED AT 09:34:20 ON 17 MAY 2006)

FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 09:34:47 ON 17 MAY 2006

L1 21 S PRO211

L2 8 S L1 AND PY=<1997